

SEQUENCE LISTING

10/581551

AP20 Rec'd PCTO 02 JUN 2006

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<120> Fluorescent protein

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<212> PRT

<213> Fungia sp.

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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130	135	140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val		
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe		160
	165	170
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser		175
	180	185
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		190
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<213> *Fungia* sp.

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
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aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	

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tgt tac ggc cac aga cct ttt act aaa tat cca gaa gag ata cca gac	240		
Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
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tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288		
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
	85	90	95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336		
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
	100	105	110
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	115	120	125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
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aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc	576		
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
	180	185	190
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			

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Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
	115	120	125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
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 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
 165 170 175
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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 Glu Leu Val Glu Asp Ala Val Ala His Ser
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 20 25 30
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
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 35 40 45
 aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
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Glu Leu Val Glu Asp Ala Val Ala His Ser

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Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

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Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

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90

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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met			
	165	170	175
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
	180	185	190
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
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Glu Leu Val Glu Asp Ala Val Ala His Ser			

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly	
20 25 30	
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc	144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala	
35 40 45	
aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc	192
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe	
50 55 60	
ggg tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac	240

Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
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 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
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 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
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 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp
 145 150 155 160
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 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met
 165 170 175
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
 180 185 190
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

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45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

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95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

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105

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
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aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

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	85	90	95
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
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cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
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cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
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gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			

	165		170		175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp					
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His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr					
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Glu Leu Val Glu Asp Ala Val Ala His Ser					
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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly					
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Arg Pro Tyr Glu Gly His Gln Glu Leu Thr Leu Arg Val Thr Met Ala					
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Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe					
50 55 60					
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Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp					
65 70 75 80					

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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
100 105 110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
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Trp Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe	
165 170 175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
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Glu Leu Val Glu Asp Ala Val Ala His Ser	
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<212> PRT

<213> Fungia sp.

<400> 11

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Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
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Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
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Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
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Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
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Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
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Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

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His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

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Glu Leu Val Glu Asp Ala Val Ala His Ser

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215

<210> 12

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<212> DNA

<213> *Fungia* sp.

<400> 12

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Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

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Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

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 85 90 95
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
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 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
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 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
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<210> 13

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<400> 13

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20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Ala Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180	185	190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		
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Glu Leu Val Glu Asp Ala Val Ala His Ser		
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85	90	95	
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggg cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
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<211> 218			

<212> PRT

<213> Fungia sp.

<400> 15

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35				40					45				
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Ser	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65				70					75					80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85					90					95		
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
		100					105						110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135						140			
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145				150					155					160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
			165					170					175		
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
		180						185					190		

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 16

<211> 657

<212> DNA

<213> Fungia sp.

<400> 16

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga tct ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Ser Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 17

<211> 218

<212> PRT

<213> Fungia sp.

<400> 17

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25						30	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
			35					40						45	
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
			50				55							60	
Cys	Tyr	Gly	His	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65					70					75					80
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
				85					90						95
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
				100					105						110
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
				115					120						125
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
			130				135							140	
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145					150					155					160
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170						175
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
				180					185						190
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr

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 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215
 <210> 18
 <211> 657
 <212> DNA
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 1 5 10 15
 ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 tgt tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser
 210 215

<210> 19

<211> 218

<212> PRT

<213> Fungia sp.

<400> 19

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 20

<211> 657

<212> DNA

<213> *Fungia* sp.

<400> 20

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga act ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384		
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576		
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624		
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657		
Glu Leu Val Glu Asp Ala Val Ala His Ser			

210 215

<210> 21

<211> 218

<212> PRT

<213> Fungia sp.

<400> 21

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
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Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65				70					75					80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85					90					95		
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100					105					110		
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145				150					155					160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
			165					170					175		
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
			180					185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
		195				200							205		
Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						

210 215

<210> 22

<211> 657

<212> DNA

<213> *Fungia* sp.

<400> 22

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

tgt tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115

120

125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130

135

140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145

150

155

160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165

170

175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180

185

190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

gag ctg gta gaa gat gca gta gct cat tcc taa

657

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 23

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 23

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			
20	25	30	
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala			
35	40	45	
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe			
50	55	60	
Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		

<210> 24

<211> 657

<212> DNA

<213> Fungia sp.

<400> 24

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

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10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga ctt ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val
 145 150 155 160
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe
 165 170 175
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp
 180 185 190
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr
 195 200 205
 gag ctg gta gaa gat gca gta gct cat tcc taa 657
 Glu Leu Val Glu Asp Ala Val Ala His Ser

210 215
 <210> 25
 <211> 218
 <212> PRT
 <213> *Fungia* sp.
 <400> 25

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
				20					25					30	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
			35					40					45		
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
		50					55						60		
Cys	Tyr	Gly	His	Arg	Tyr	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
	65					70					75				80
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
				85					90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100						105					110	
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
			115					120					125		
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
		130					135					140			
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
	145					150					155				160
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
				180					185					190	
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
			195					200					205		
Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						
		210					215								

<210> 26

<211> 657

<212> DNA

<213> *Fungia* sp.

<400> 26

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga tac ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
	165	170	175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576		
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
	180	185	190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624		
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
	195	200	205
gag ctg gta gaa gat gca gta gct cat tcc taa			657
Glu Leu Val Glu Asp Ala Val Ala His Ser			

<210> 27

<211> 218

<212> PRT

<213> Fungia sp.

<400> 27

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1	5	10	15
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20	25	30
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala		
35	40	45
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe		
50	55	60
Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp		
65	70	75
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu		
85	90	95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu		
100	105	110
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe		
115	120	125
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro		
130	135	140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val		
145	150	155
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe		
165	170	175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp		
180	185	190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		
195	200	205
Glu Leu Val Glu Asp Ala Val Ala His Ser		
210	215	
<210> 28		
<211> 657		

<212> DNA

<213> Fungia sp.

<400> 28

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
      1              5              10              15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
              20              25              30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
              35              40              45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
              50              55              60
tgt tac ggc cac aga cag ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
              65              70              75              80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
              85              90              95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
              100              105              110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
              115              120              125
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cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130

135

140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145

150

155

160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165

170

175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180

185

190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

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gag ctg gta gaa gat gca gta gct cat tcc taa

657

Glu Leu Val Glu Asp Ala Val Ala His Ser

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215

<210> 29

<211> 218

<212> PRT

<213> Fungia sp.

<220>

<221> UNSURE

<222> (186)

<223> unknown amiono acid

<400> 29

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			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35					40					45			
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Asn	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65				70					75					80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85					90					95		
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
		100					105					110			
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115					120				125				
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145				150					155					160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
			165					170					175		
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Xaa	Leu	Glu	Met	Pro	Gly	Asp
		180						185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
		195				200						205			
Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						

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<210> 30

<211> 657

<212> DNA

<213> *Fungia* sp.

<220>

<221> unsure

<222> (556)

<223> unknown nucleotide

<400> 30

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

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ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga aat ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85	90	95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336			
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag ntt ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 31			
<211> 665			

<212> PRT

<213> Fungia sp.

<400> 31

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			20					25						30	
Gln	Asp	Gln	Glu	Gly	Asp	Thr	Asp	Ala	Gly	Leu	Lys	Glu	Ser	Pro	Leu
		35					40					45			
Gln	Thr	Pro	Thr	Glu	Asp	Gly	Ser	Glu	Glu	Pro	Gly	Ser	Glu	Thr	Ser
	50					55					60				
Asp	Ala	Lys	Ser	Thr	Pro	Thr	Ala	Glu	Asp	Val	Thr	Ala	Pro	Leu	Val
65				70					75					80	
Asp	Glu	Gly	Ala	Pro	Gly	Lys	Gln	Ala	Ala	Ala	Gln	Pro	His	Thr	Glu
				85					90					95	
Ile	Pro	Glu	Gly	Thr	Thr	Ala	Glu	Glu	Ala	Gly	Ile	Gly	Asp	Thr	Pro
		100						105						110	
Ser	Leu	Glu	Asp	Glu	Ala	Ala	Gly	His	Val	Thr	Gln	Ala	Arg	Met	Val
		115					120					125			
Ser	Lys	Ser	Lys	Asp	Gly	Thr	Gly	Ser	Asp	Asp	Lys	Lys	Ala	Lys	Gly
	130					135					140				
Ala	Asp	Gly	Lys	Thr	Lys	Ile	Ala	Thr	Pro	Arg	Gly	Ala	Ala	Pro	Pro
145				150					155					160	
Gly	Gln	Lys	Gly	Gln	Ala	Asn	Ala	Thr	Arg	Ile	Pro	Ala	Lys	Thr	Pro
			165					170						175	
Pro	Ala	Pro	Lys	Thr	Pro	Pro	Ser	Ser	Gly	Glu	Pro	Pro	Lys	Ser	Gly
		180						185						190	

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
 195 200 205
 Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
 210 215 220
 Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
 225 230 235 240
 Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
 245 250 255
 Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
 260 265 270
 Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
 275 280 285
 Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
 290 295 300
 Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
 305 310 315 320
 Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
 325 330 335
 Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
 340 345 350
 Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
 355 360 365
 Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
 370 375 380
 Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
 385 390 395 400
 Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser

	405	410	415
Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val			
	420	425	430
Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met			
	435	440	445
Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly			
	450	455	460
Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg			
465	470	475	480
Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu			
	485	490	495
Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys			
	500	505	510
Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr			
	515	520	525
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu			
	530	535	540
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg			
545	550	555	560
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro			
	565	570	575
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser			
	580	585	590
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr			
	595	600	605
Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys			
	610	615	620

Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His

625 630 635 640

Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu

645 650 655

Leu Val Glu Asp Ala Val Ala His Ser

660 665

<210> 32

<211> 1998

<212> DNA

<213> *Fungia* sp.

<400> 32

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Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly

1 5 10 15

acg tac ggg ttg ggg gac agg aaa gat cag ggg ggc tac acc atg cac 96

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His

20 25 30

caa gac caa gag ggt gac acg gac gct ggc ctg aaa gaa tct ccc ctg 144

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu

35 40 45

cag acc ccc act gag gac gga tct gag gaa ccg ggc tct gaa acc tct 192

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser

50 55 60

gat gct aag agc act cca aca gcg gaa gat gtg aca gca ccc tta gtg 240

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val

65 70 75 80

gat gag gga gct ccc ggc aag cag gct gcc gcg cag ccc cac acg gag 288

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
 85 90 95
 atc cca gaa gga acc aca gct gaa gaa gca ggc att gga gac acc ccc 336
 Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
 100 105 110
 agc ctg gaa gac gaa gct gct ggt cac gtg acc caa gct cgc atg gtc 384
 Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
 115 120 125
 agt aaa agc aaa gac ggg act gga agc gat gac aaa aaa gcc aag ggg 432
 Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
 130 135 140
 gct gat ggt aaa acg aag atc gcc aca ccg cgg gga gca gcc cct cca 480
 Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
 145 150 155 160
 ggc cag aag ggc cag gcc aac gcc acc agg att cca gca aaa acc ccg 528
 Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
 165 170 175
 ccc gct cca aag aca cca ccc agc tct ggt gaa cct cca aaa tca ggg 576
 Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
 180 185 190
 gat cgc agc ggc tac agc agc ccc ggc tcc cca ggc act ccc ggc agc 624
 Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
 195 200 205
 cgc tcc cgc acc ccg tcc ctt cca acc cca ccc acc cgg gag ccc aag 672
 Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
 210 215 220
 aag gtg gca gtg gtc cgt act cca ccc aag tcg ccg tct tcc gcc aag 720

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
 225 230 235 240
 agc cgc ctg cag aca gcc ccc gtg ccc atg cca gac ctg aag aat gtc 768
 Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
 245 250 255
 aag tcc aag atc ggc tcc act gag aac ctg aag cac cag ccg gga ggc 816
 Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
 260 265 270
 ggg aag gtg cag ata att aat aag aag ctg gat ctt agc aac gtc cag 864
 Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
 275 280 285
 tcc aag tgt ggc tca aag gat aat atc aaa cac gtc ccg gga ggc ggc 912
 Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
 290 295 300
 agt gtg caa ata gtc tac aaa cca gtt gac ctg agc aag gtg acc tcc 960
 Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
 305 310 315 320
 aag tgt ggc tca tta ggc aac atc cat cat aaa cca gga ggt ggc cag 1008
 Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
 325 330 335
 gtg gaa gta aaa tct gag aag ctt gac ttc aag gac aga gtc cag tcg 1056
 Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
 340 345 350
 aag att ggg tcc ctg gac aat atc acc cac gtc cct ggc gga gga aat 1104
 Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
 355 360 365
 aaa aag att gaa acc cac aag ctg acc ttc cgc gag aac gcc aaa gcc 1152

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
 370 375 380
 aag aca gac cac ggg gcg gag atc gtg tac aag tcg cca gtg gtg tct 1200
 Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
 385 390 395 400
 ggg gac acg tct cca cgg cat ctc agc aat gtc tcc tcc acc ggc agc 1248
 Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
 405 410 415
 atc gac atg gta gac tcg ccc cag ctc gcc acg cta gct gac gag gtg 1296
 Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
 420 425 430
 tct gcc tcc ctg gcc aag cag ggt ttg gga tcc gga ggt gaa ttc atg 1344
 Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met
 435 440 445
 gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac ggc 1392
 Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly
 450 455 460
 tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc aga 1440
 Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg
 465 470 475 480
 cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc gag 1488
 Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu
 485 490 495
 ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc tgt 1536
 Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys
 500 505 510
 tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac tat 1584

Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr
515 520 525
ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg gag 1632
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu
530 535 540
ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt aga 1680
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg
545 550 555 560
gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt cct 1728
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro
565 570 575
gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca tca 1776
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser
580 585 590
acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt acg 1824
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr
595 600 605
atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc aag 1872
Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys
610 615 620
act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac cat 1920
Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His
625 630 635 640
tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act gag 1968
Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu
645 650 655
ctg gta gaa gat gca gta gct cat tcc taa 1998

Leu Val Glu Asp Ala Val Ala His Ser

660

665

<210> 33

<211> 480

<212> PRT

<213> Fungia sp.

<400> 33

Met Gly Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys

1

5

10

15

Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn

20

25

30

Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn

35

40

45

Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp

50

55

60

Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val

65

70

75

80

Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg

85

90

95

Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu

100

105

110

Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg

115

120

125

Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys

130

135

140

Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val

145

150

155

160

Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser			
165	170	175	
Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met			
180	185	190	
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn			
195	200	205	
Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp			
210	215	220	
Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys			
225	230	235	240
Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg			
245	250	255	
Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys			
260	265	270	
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile			
275	280	285	
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr			
290	295	300	
Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp			
305	310	315	320
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr			
325	330	335	
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu			
340	345	350	
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val			
355	360	365	
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys			

370	375	380	
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
385	390	395	400
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly			
	405	410	415
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly			
	420	425	430
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile			
	435	440	445
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys			
	450	455	460
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser			
465	470	475	480

<210> 34

<211> 1443

<212> DNA

<213> Fungia sp.

<400> 34

atg gga acc atc ctt ttc ctt act atg gtt att tca tac ttc ggt tgc 48

Met Gly Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys

1	5	10	15
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atg aag gct gcg ccc atg aaa gaa gca aac gtc cac gga caa ggc aac 96

Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn

20	25	30
----	----	----

ttg gcc tac cca gct gtg cgg acc cat ggg act ctg gag agc gtg aat 144

Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn

35	40	45
----	----	----

ggg ccc agg gca ggt tcg aga ggt ctg acg acg acg tcc ctg gct gac 192
 Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp
 50 55 60
 act ttt gag cac gtg atc gaa gag ctg ctg gat gag gac cag aag gtt 240
 Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val
 65 70 75 80
 cgg ccc aac gaa gaa aac cat aag gac gcg gac ttg tac act tcc cgg 288
 Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg
 85 90 95
 gtg atg ctc agc agt caa gtg cct ttg gag cct cct ctg ctc ttt ctg 336
 Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu
 100 105 110
 ctg gag gaa tac aaa aat tac ctg gat gcc gca aac atg tct atg agg 384
 Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg
 115 120 125
 gtt cgg cgc cac tcc gac ccc gcc cgc cgt ggg gag ctg agc gtg tgt 432
 Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys
 130 135 140
 gac agt att agc gag tgg gtc aca gcg gca gat aaa aag act gca gtg 480
 Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val
 145 150 155 160
 gac atg tcc ggt ggg acg gtc aca gtc ctg gag aaa gtc ccg gta tca 528
 Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser
 165 170 175
 aaa ggc caa ctg aag caa tat ttc tac gag acc aag tgt aat ccc atg 576
 Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met
 180 185 190

ggt tac acg aag gaa ggc tgc agg ggc ata gac aaa agg cac tgg aac 624
 Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn
 195 200 205
 tcg caa tgc cga act acc caa tcg tat gtt cgg gcc ctt act atg gat 672
 Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp
 210 215 220
 agc aaa aag aga att ggc tgg cgg ttc ata agg ata gac act tcc tgt 720
 Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys
 225 230 235 240
 gta tgt aca ctg acc att aaa agg gga aga ggg gta ccg cgg gcc cgg 768
 Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg
 245 250 255
 gac cca ccg gtc gcc acc atg gtg agt gtg att aaa cca gag atg aag 816
 Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys
 260 265 270
 atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 864
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 275 280 285
 gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 912
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 290 295 300
 cta cgc gtc aca atg gcc gag ggc ggg cca atg cct ttc gcg ttt gac 960
 Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp
 305 310 315 320
 tta gtg tca cac gtg ttc tgt tac ggc cac aga gta ttt act aaa tat 1008
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr
 325 330 335

cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1056
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
340 345 350

tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1104
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
355 360 365

agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1152
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
370 375 380

ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1200
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
385 390 395 400

agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1248
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
405 410 415

gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1296
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
420 425 430

aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa gag att 1344
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile
435 440 445

ctt gaa atg cca gga gac cat tac atc ggc cat cgc ctc gtc agg aaa 1392
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys
450 455 460

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1440
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
465 470 475 480

taa

1443

<210> 35

<211> 464

<212> PRT

<213> Fungia sp.

<400> 35

Met Val Ser Tyr Ser Lys Gln Gly Ile Ala Gln Glu Met Arg Thr Lys

1

5

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15

Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly

20

25

30

Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val

35

40

45

Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu

50

55

60

Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala

65

70

75

80

Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr

85

90

95

Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp

100

105

110

Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His

115

120

125

Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile

130

135

140

Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu

145

150

155

160

Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln

	165	170	175
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met			
	180	185	190
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly			
	195	200	205
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala			
	210	215	220
His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val			
225	230	235	240
Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys			
	245	250	255
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile			
	260	265	270
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr			
	275	280	285
Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp			
	290	295	300
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr			
305	310	315	320
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu			
	325	330	335
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val			
	340	345	350
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys			
	355	360	365
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
	370	375	380

Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400

Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415

Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430

Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445

Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
 450 455 460

<210> 36

<211> 1395

<212> DNA

<213> Fungia sp.

<400> 36

atg gtg tct tat tca aag caa ggc atc gca caa gaa atg cgg acg aaa 48

Met Val Ser Tyr Ser Lys Gln Gly Ile Ala Gln Glu Met Arg Thr Lys

1 5 10 15

tac cgt atg gaa ggc agt gtc aat ggc cat gaa ttc acg atc gaa ggt 96

Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly

20 25 30

gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144

Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val

35 40 45

atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192

Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu

50 55 60

tca	aca	gcc	ttt	caa	tat	gga	aac	aga	tgc	ttc	aca	aag	tac	cct	gca	240
Ser	Thr	Ala	Phe	Gln	Tyr	Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala	
65						70						75				80
gac	atg	cct	gac	tat	ttc	aag	caa	gca	ttc	cca	gat	gga	atg	tca	tat	288
Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr	
						85						90				95
gaa	agg	tca	ttt	cta	ttt	gag	gat	gga	gga	gtt	gct	aca	gcc	agc	tgg	336
Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp	
						100						105				110
agc	att	cgt	ctc	gaa	gga	aat	tgc	ttc	atc	cac	aat	tcc	atc	tat	cat	384
Ser	Ile	Arg	Leu	Glu	Gly	Asn	Cys	Phe	Ile	His	Asn	Ser	Ile	Tyr	His	
						115						120				125
ggc	gta	aac	ttt	ccc	gct	gat	gga	ccc	gta	atg	aag	aag	cag	aca	att	432
Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Gln	Thr	Ile	
						130						135				140
ggc	tgg	gat	aag	tcc	ttc	gaa	aaa	atg	agt	gtg	gct	aaa	gag	gtg	cta	480
Gly	Trp	Asp	Lys	Ser	Phe	Glu	Lys	Met	Ser	Val	Ala	Lys	Glu	Val	Leu	
145												150				155
aga	ggt	gat	gtg	act	cag	ttt	ctt	ctg	ctc	gaa	gga	ggt	ggt	tac	cag	528
Arg	Gly	Asp	Val	Thr	Gln	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Gln	
																165
																170
																175
aga	tgc	cgg	ttt	cac	tcc	act	tac	aaa	acg	gag	aag	cca	gtc	gca	atg	576
Arg	Cys	Arg	Phe	His	Ser	Thr	Tyr	Lys	Thr	Glu	Lys	Pro	Val	Ala	Met	
																180
																185
																190
ccc	ccg	agt	cat	gtc	gta	gaa	cat	caa	att	gtg	agg	acc	gac	ctt	ggc	624
Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly	
																195
																200
																205

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
 210 215 220
 cat gtt aac cct ttg aag gtt aaa ggt ggc agc ggt ggc gac gag gtg 720
 His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val
 225 230 235 240
 gac ggt acc ggt ggc agc atg gtg agt gtg att aaa cca gag atg aag 768
 Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys
 245 250 255
 atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 816
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile
 260 265 270
 gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 864
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr
 275 280 285
 cta cgc gtc aca atg gcc aag ggc ggg cca atg cct ttc gcg ttt gac 912
 Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp
 290 295 300
 tta gtg tca cac gtg ttc tgt tac ggc cac aga cct ttt act aaa tat 960
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr
 305 310 315 320
 cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1008
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu
 325 330 335
 tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1056
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val
 340 345 350

agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1104
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys
 355 360 365
 ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1152
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln
 370 375 380
 agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1200
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly
 385 390 395 400
 gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1248
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly
 405 410 415
 aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa aag att 1296
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile
 420 425 430
 ctt aaa atg cca gga agc cat tac atc agc cat cgc ctc gtc agg aaa 1344
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys
 435 440 445
 acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1392
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser
 450 455 460
 taa 1395

<210> 37

<211> 221

<212> PRT

<213> *Montipora. sp*

<400> 37

Met	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	Gly
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Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	Lys
			20					25					30		
Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	Gly
			35				40					45			
Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Ser	Gln	Tyr	Gly
	50					55					60				
Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	Lys
65					70					75				80	
Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Ile	Met	His	Phe	Glu
				85					90					95	
Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	Asn
			100					105					110		
Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Val	Asn	Phe	Pro	Pro	Asn
			115				120					125			
Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Asn	Thr	Glu
	130					135					140				
Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asn	Phe	Met	Ala
145					150					155				160	
Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser	Thr
				165					170				175		
Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Val	Asp
			180					185					190		
Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Lys	Asp	Tyr	Thr	Phe	Val	Glu
			195				200					205			
Gln	Cys	Glu	Ile	Ser	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly			

210	215	220
<210> 38		
<211> 666		
<212> DNA		
<213> <i>Montipora. sp</i>		
<400> 38		
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Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly		
1	5	10 15
acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96		
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys		
20	25	30
cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggt gga 144		
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly		
35	40	45
cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac gga 192		
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly		
50	55	60
agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag 240		
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys		
65	70	75 80
cag tca ttc cct gag gga tat aca tgg gag agg atc atg cac ttt gaa 288		
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu		
85	90	95
gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336		
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn		
100	105	110

tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc aat 384

Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn

115

120

125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag 432

Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu

130

135

140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct 480

Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala

145

150

155

160

ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act 528

Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr

165

170

175

tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac 576

Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp

180

185

190

cgc aaa ctg gat gta acc agt cac aac aag gat tac aca ttt gtt gag 624

Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu

195

200

205

cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 666

Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly

210

215

220

<210> 39

<211> 222

<212> PRT

<213> *Montipora. sp*

<400> 39

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

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Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly			
20	25	30	
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly			
35	40	45	
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr			
50	55	60	
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val			
65	70	75	80
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe			
85	90	95	
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly			
100	105	110	
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro			
115	120	125	
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met			
145	150	155	160
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
165	170	175	
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val			
180	185	190	
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly			
210	215	220	

<210> 40

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 40

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Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

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15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

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25

30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

35

40

45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr

50

55

60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65

70

75

80

aag cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe

85

90

95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100

105

110

aac tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro
 115 120 125
 aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr
 130 135 140
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat ttt atg 480
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met
 145 150 155 160
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct 528
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser
 165 170 175
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt 576
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val
 180 185 190
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val
 195 200 205
 gag cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 669
 Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly
 210 215 220
 <210> 41
 <211> 222
 <212> PRT
 <213> *Montipora. sp*
 <400> 41
 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
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Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly
			20					25						30	
Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly
			35					40						45	
Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Phe	Gln	Tyr
			50					55						60	
Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val
			65					70						75	80
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe
								85						90	95
Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly
								100						105	110
Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro
								115						120	125
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr
								130						135	140
Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	Met
								145						150	155
Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser
								165						170	175
Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Ile
								180						185	190
Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	Val
								195						200	205
Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly		
								210						215	220

<210> 42

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 42

atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca 48

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

1

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15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

20

25

30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

35

40

45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr

50

55

60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65

70

75

80

aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe

85

90

95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100

105

110

aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro

115	120	125	
aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480			
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met			
145	150	155	160
gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528			
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
	165	170	175
act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576			
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile			
	180	185	190
gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624			
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669			
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			
210	215	220	
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<212> PRT			
<213> <i>Montipora. sp</i>			
<400> 43			
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser			
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Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly			

	20		25		30										
Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly
	35		40		45										
Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Met	Cys	Tyr
	50		55		60										
Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val
65			70		75									80	
Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Met	Asn	Phe
	85		90		95										
Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly
	100		105		110										
Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Thr	Asn	Phe	Pro	Pro
	115		120		125										
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser	Thr
	130		135		140										
Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr	Met
145			150		155									160	
Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser
	165		170		175										
Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Ile
	180		185		190										
Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser	Val
	195		200		205										
Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly		
	210		215		220										

<210> 44

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 44

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1 5 10 15
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Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
20 25 30
aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
35 40 45
gga cct ctg cca ttt gct tgg gat att tta tca cca ctg atg tgt tac 192
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr
50 55 60
gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
65 70 75 80
aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
85 90 95
gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
100 105 110
aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
115 120 125

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432

Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr

130

135

140

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480

Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met

145

150

155

160

gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528

Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser

165

170

175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576

Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile

180

185

190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624

Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val

195

200

205

gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669

Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

210

215

220

<210> 45

<211> 255

<212> PRT

<213> *Montipora. sp*

<400> 45

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20

25

30

Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met			
35	40	45	
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys			
50	55	60	
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys			
65	70	75	80
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln			
85	90	95	
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr			
100	105	110	
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn			
115	120	125	
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln			
130	135	140	
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro			
145	150	155	160
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser			
165	170	175	
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr			
180	185	190	
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys			
195	200	205	
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu			
210	215	220	
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser			
225	230	235	240
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			

245	250	255
<210> 46		
<211> 765		
<212> DNA		
<213> <i>Montipora. sp</i>		
<400> 46		
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1	5	10
ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96		
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp		
20	25	30
ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144		
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met		
35	40	45
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192		
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys		
50	55	60
gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240		
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys		
65	70	75
ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ttc cag 288		
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln		
85	90	95
tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336		
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr		
100	105	110

ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu
 210 215 220
 att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 245 250 255

<210> 47

<211> 255

<212> PRT

<213> *Montipora. sp*

<400> 47

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr
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				20				25						30	
Pro	Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met
				35				40						45	
Ser	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys
				50				55						60	
Gly	Lys	Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys
				65				70						75	
															80
Gly	Gly	Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Gln	Leu	Gln
				85						90				95	
Tyr	Gly	Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr
				100						105				110	
Phe	Lys	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Ser	Met	Asn
				115						120				125	
Phe	Glu	Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln
				130						135				140	
Gly	Asn	Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Glu	Asn	Phe	Pro
				145						150				155	
															160
Pro	Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Ser
				165						170				175	

Thr	Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr
180					185					190					
Met	Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys
195					200					205					
Ser	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Arg	His	Glu
210					215					220					
Ile	Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser
225			230				235				240				
Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	
245					250					255					

<210> 48

<211> 765

<212> DNA

<213> *Montipora. sp*

<400> 48

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1	5				10				15							
ggt	gga	cag	caa	atg	ggt	cgg	gat	ctg	tac	gac	gat	gac	gat	aag	gat	96
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp	
20				25				30								
ccc	atg	gtg	agt	gtg	atc	gct	aaa	caa	atg	acc	tac	aag	gtt	tat	atg	144
Pro	Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	
35				40				45								
tca	ggc	acg	gtc	aat	gga	cac	tac	ttt	gag	gtc	gaa	ggc	gat	gga	aaa	192
Ser	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	
50				55				60								

gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80
 ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ctt cag 288
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln
 85 90 95
 tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn
 115 120 125
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro
 145 150 155 160
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205

tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672

Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu

210

215

220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720

Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser

225

230

235

240

gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765

Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

245

250

255

<210> 49

<211> 747

<212> PRT

<213> *Montipora. sp*

<400> 49

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35

40

45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

55

60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65

70

75

80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85

90

95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly	
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
225	230	235
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr		
245	250	255
Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser		
260	265	270
Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly		
275	280	285
Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg		
290	295	300
Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly		
305	310	315
		320

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly
 325 330 335
 Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys
 340 345 350
 Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu
 355 360 365
 Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
 370 375 380
 Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
 385 390 395 400
 Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
 405 410 415
 Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
 420 425 430
 Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
 435 440 445
 Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
 450 455 460
 Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
 465 470 475 480
 Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu
 485 490 495
 Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly
 500 505 510
 Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp
 515 520 525
 Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val

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Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr			
545	550	555	560
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu			
	565	570	575
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys			
	580	585	590
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser			
	595	600	605
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly			
610	615	620	
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe			
625	630	635	640
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro			
	645	650	655
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met			
	660	665	670
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys			
	675	680	685
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met			
690	695	700	
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys			
705	710	715	720
Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr			
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Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala			
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<211> 2241

<212> DNA

<213> *Montipora. sp*

<400> 50

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc 720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225 230 235 240
gga ctc aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc 768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr
245 250 255
gcg ggc ccg ctg tac gac gaa gtc gat aag gat ccg atg gcc tcc tcc 816

Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser
 260 265 270
 gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc 864
 Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly
 275 280 285
 tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc 912
 Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg
 290 295 300
 ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc 960
 Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly
 305 310 315 320
 ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc 1008
 Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly
 325 330 335
 tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag 1056
 Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys
 340 345 350
 ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag 1104
 Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu
 355 360 365
 gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc 1152
 Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
 370 375 380
 gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac 1200
 Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
 385 390 395 400
 ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag 1248

Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr			
545	550	555	560
gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg 1728			
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu			
	565	570	575
ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag 1776			
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys			
	580	585	590
gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc 1824			
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser			
	595	600	605
ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc 1872			
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly			
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Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe			
625	630	635	640
atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc 1968			
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro			
	645	650	655
gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg 2016			
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met			
	660	665	670
tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag 2064			
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys			
	675	680	685
ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg 2112			

Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
 690 695 700
 gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag 2160
 Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
 705 710 715 720
 ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac 2208
 Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
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 Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 35 40 45
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 50 55 60
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 65 70 75 80
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

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Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
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Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
	115	120	125
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
	130	135	140
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
	145	150	155
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
	165	170	175
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
	180	185	190
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
	195	200	205
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
	210	215	220
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
	225	230	235
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
	245	250	255
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	260	265	270
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser			
	275	280	285
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val			
	290	295	300

Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr			
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Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile			
	340	345	350
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser			
	355	360	365
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly			
	370	375	380
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe			
385	390	395	400
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro			
	405	410	415
Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu			
	420	425	430
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys			
	435	440	445
Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys			
	450	455	460
Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys			
465	470	475	480
Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys			
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<211> 1521

<212> DNA

<213> *Montipora. sp*

<400> 52

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
              20              25              30
ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144
Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
              35              40              45
ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc 192
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
              50              55              60
ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
              65              70              75              80
atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
              85              90              95
acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336
Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
              100              105              110
aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
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115	120	125	
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432			
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
130	135	140	
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480			
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
145	150	155	160
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528			
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
	165	170	175
tac aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576			
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
	180	185	190
aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc 624			
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
195	200	205	
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672			
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
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Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
225	230	235	240
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768			
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
	245	250	255
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 816			
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			

260	265	270	
tcc tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agt	864		
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser			
275	280	285	
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Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val			
290	295	300	
aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct tac	960		
Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr			
305	310	315	320
gag gga gag cag aca gta aag ctc act gtc acc aag ggt gga cct ctg	1008		
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu			
325	330	335	
cca ttt gct tgg gat att tta tca cca ctg ttt cag tac gga agc ata	1056		
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile			
340	345	350	
cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag cag tca	1104		
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser			
355	360	365	
ttc cct gag gga tat aca tgg gag agg acc atg aac ttt gaa gat ggt	1152		
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly			
370	375	380	
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Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe			
385	390	395	400
atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc aat gga cct	1248		
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro			

405	410	415	
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420	425	430	
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435	440	445	
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450	455	460	
gca aag aag cct gtg agg atg cca ggg tat cac tat att gac cgc aaa 1440			
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465	470	475	480
ctg gat gta acc agt cac aac agg gat tac aca tct gtt gag cag tgt 1488			
Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys			
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gaa ata gcc att gca cgc cac tct ttg ctc ggt			1521
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	35		40		45
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys					
	50		55		60
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys					
	65		70		75
					80
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln					
		85		90	
					95
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr					
	100		105		110
Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn					
	115		120		125
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln					
	130		135		140
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro					
	145		150		155
					160
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser					
		165		170	
					175
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr					
	180		185		190
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys					
	195		200		205
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr					
	210		215		220
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser					
	225		230		235
					240

Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	Ser
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Ser	Ser	Glu	Leu	Ser	Gly	Asp	Glu	Val	Asp	Gly	Thr	Met	Val	Ser	Lys
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Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Trp	Gly
			325						330					335	
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe
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Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu
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Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys
385				390						395				400	
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Ile	Ser
			405						410					415	
His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala
		420						425					430		
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala
		435					440						445		
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu

450 455 460
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
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 485 490 495
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<211> 1521

<212> DNA

<213> *Montipora. sp*

<400> 54

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 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
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 ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met
 35 40 45
 tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys
 50 55 60
 gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys
 65 70 75 80

ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag 288
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln
 85 90 95
 tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr
 100 105 110
 gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac 384
 Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn
 115 120 125
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln
 130 135 140
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct 480
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro
 145 150 155 160
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser
 165 170 175
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr
 180 185 190
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys
 195 200 205
 tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat 672
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr
 210 215 220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser
 225 230 235 240
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tcc 768
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser
 245 250 255
 tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agc aag 816
 Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys
 260 265 270
 ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac 864
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 275 280 285
 ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc 912
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 290 295 300
 gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc 960
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 305 310 315 320
 aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc 1008
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly
 325 330 335
 gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc 1056
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe
 340 345 350
 ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc 1104
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 355 360 365

ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag 1152
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 370 375 380
 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 1200
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 385 390 395 400
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 1248
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser
 405 410 415
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 1296
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 420 425 430
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1344
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 435 440 445
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1392
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 450 455 460
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1440
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 465 470 475 480
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1488
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 485 490 495
 ggg atc act ctc ggc atg gac gag ctg tac aag 1521
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 500 505

<210> 55

<211> 411

<212> PRT

<213> *Montipora. sp*

<400> 55

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr
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Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp
				20				25						30	
Pro	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile
				35				40						45	
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser
				50				55				60			
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe
				65				70				75			80
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr
				85						90				95	
Thr	Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met
				100						105				110	
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln
				115						120				125	
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala
				130						135				140	
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys
				145						150				155	
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu
				165						170				175	

Tyr	Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys
180				185				190							
Asn	Gly	Ile	Lys	Ala	His	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly
195				200				205							
Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp
210				215				220							
Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala
225				230				235				240			
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu
245				250				255							
Phe	Val	Thr	Ala	Ala	Arg	Met	His	Asp	Gln	Leu	Thr	Glu	Glu	Gln	Ile
260				265				270							
Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	Leu	Phe	Asp	Lys	Asp	Gly	Asp	Gly
275				280				285							
Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	Thr	Val	Met	Arg	Ser	Leu	Gly	Gln
290				295				300							
Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met	Ile	Asn	Glu	Val	Asp	Ala
305				310				315				320			
Asp	Gly	Asn	Gly	Thr	Ile	Tyr	Phe	Pro	Glu	Phe	Leu	Thr	Met	Met	Ala
325				330				335							
Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu	Glu	Ile	Arg	Glu	Ala	Phe
340				345				350							
Arg	Val	Phe	Asp	Lys	Asp	Gly	Asn	Gly	Tyr	Ile	Ser	Ala	Ala	Glu	Leu
355				360				365							
Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu	Lys	Leu	Thr	Asp	Glu	Glu	Val
370				375				380							
Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Ile	Asp	Gly	Asp	Gly	Gln	Val	Asn

385 390 395 400

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys

405 410

<210> 56

<211> 1233

<212> DNA

<213> *Montipora. sp*

<400> 56

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1 5 10 15

ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20 25 30

ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144

Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile

35 40 45

ctg gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc 192

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser

50 55 60

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

65 70 75 80

atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

85 90 95

acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336

Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 100 105 110
 aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 115 120 125
 gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 130 135 140
 gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 145 150 155 160
 ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 165 170 175
 tac aac tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 180 185 190
 aac ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc 624
 Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 195 200 205
 agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 210 215 220
 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 720
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 225 230 235 240
 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 245 250 255
 ttc gtg acc gcc gcc cgc atg cat gac caa ctg aca gaa gag cag att 816
 Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile
 260 265 270
 gca gag ttc aaa gaa gcc ttc tca tta ttc gac aag gat ggg gac ggc 864
 Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly
 275 280 285
 acc atc acc aca aag gaa ctt ggc acc gtt atg agg tcg ctt gga caa 912
 Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln
 290 295 300
 aac cca acg gaa gca gaa ttg cag gat atg atc aat gaa gtc gat gct 960
 Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala
 305 310 315 320
 gat ggc aat gga acg att tac ttt cct gaa ttt ctt act atg atg gct 1008
 Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala
 325 330 335
 aga aaa atg aag gac aca gac agc gaa gag gaa atc cga gaa gca ttc 1056
 Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe
 340 345 350
 cgt gtt ttt gac aag gat ggg aac ggc tac atc agc gct gct gaa tta 1104
 Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu
 355 360 365
 cgt cac gtc atg aca aac ctc ggg gag aag tta aca gat gaa gaa gtt 1152
 Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val
 370 375 380
 gat gaa atg ata agg gaa gca gat atc gat ggt gat ggc caa gta aac 1200

Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn
 385 390 395 400
 tat gaa gag ttt gta caa atg atg aca gca aag 1233

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys
 405 410

<210> 57

<211> 288

<212> PRT

<213> *Montipora. sp*

<400> 57.

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30

Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn
 35 40 45

Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser
 50 55 60

Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr
 65 70 75 80

Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly
 85 90 95

Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr
 100 105 110

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe
 115 120 125

Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp

130	135	140			
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met					
145	150	155	160		
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile					
	165	170	175		
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe					
	180	185	190		
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro					
	195	200	205		
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp					
	210	215	220		
Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe					
225	230	235	240		
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His					
	245	250	255		
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr					
	260	265	270		
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly					
	275	280	285		

<210> 58

<211> 864

<212> DNA

<213> *Montipora. sp*

<400> 58

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1

5

10

15

ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
 20 25 30
 ccc aag agg cgc tgg aag aaa aac ttc att gcc gtc agc gct gcc aac 144
 Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn
 35 40 45
 cgg ttc aag aag atc tcc agc tcc ggg gca ctg gga ggt gga ggt agt 192
 Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser
 50 55 60
 gag ctc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat 240
 Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr
 65 70 75 80
 atg tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga 288
 Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly
 85 90 95
 aaa gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc 336
 Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr
 100 105 110
 aag ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt 384
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe
 115 120 125
 cag tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat 432
 Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp
 130 135 140
 tat gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg 480
 Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met
 145 150 155 160

aac ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc 528
 Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile
 165 170 175
 caa ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt 576
 Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe
 180 185 190
 cct ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc 624
 Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro
 195 200 205
 agc act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat 672
 Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp
 210 215 220
 tat atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt 720
 Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe
 225 230 235 240
 aaa tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac 768
 Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His
 245 250 255
 tat att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca 816
 Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr
 260 265 270
 tct gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 864
 Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly
 275 280 285

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 59

ccagagatga agatgaggta ctacatggac ggc

33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 60

catgagttca caattgaagg tgaaggc

27

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 61

gaaggcacag gcagacctta cgaggga

27

<210> 62

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 62

ccaatgcctt tcgcgtttga cttagtg

27

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 63

ttagtgtcac acgtgttctg ttacggc

27

<210> 64

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 64

gaaaggtcgt tggagttcga agatggg

27

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 65

gaagatgggtg ggtccgcttc agtcagtgcg

30

<210> 66

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 66

agccttagag gaaacacctt ctaccacaaa tcca

34

<210> 67

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 67

caaatccaaa tttactgggg ttaactttcc tg

32

<210> 68

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 68

gccgatggtc ctatcatgca aaaccaaagt

30

<210> 69

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 69

gccgatggtc ctatcatgca aaaccaaagt gttgattggg agcca 45

<210> 70

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 70

gagaaaatta ctgccagcga cggagttctg aag 33

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 71

gatgttacga tgtacctaaa acttgaagga ggcggcaatc ac 42

<210> 72

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 72

cttaaaatgc caggaagcca ttacatcagc catgcctcg tcagg 45

<210> 73

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 73

gatgcagtag ctcatccct cgagcaccac cacc 34

<210> 74

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 74

gaaggrtgyg tcaayggrca y 21

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 75

acvggdccat ydgvaagaaa rtt 23

<210> 76

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 76

ggccacgcgt cgactagtac gggiigggii gggiig 36

<210> 77

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 77

ctcagggaat gactgcttta cat 23

<210> 78

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 78

ggccacgcgt cgactagtac 20

<210> 79

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 79

gtcttcaggg tacttggtga 20

<210> 80

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 80

atgtaaagca gtcattccct gag 23

<210> 81

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 81

cccgatccg accatggcta ccttggttaa aga 33